SEQUENCE LISTING

<110> DING, Jeak Ling
HO, Bow

<120> Sushi Peptide Multimer

<130> 79612-60

<140> CA2432972
<141> 2003-07-04

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<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<223> Sushi-3 peptide

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His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
1 5 10 15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
20 25 30

Leu Met

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His Ala Glu His Lys Val Lys Ile Lys Val Lys Gln Lys Tyr Gly Gln
1 5 10 15

Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
20 25 30

Leu Met

<210> 3
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TCGAAGACGG CCCCAGGATC CCCATGCTGA ACACAAGG 38

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TAGAAGACCC GGGGGTCCAT CAAAGAAAGT AGTTA 35

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                   Met Val Leu Ala Ser Phe Leu Val Ser Gly Leu
                     1               5                  10

gtt cta ggg cta cta gcc caa aaa atg cgc cca gtt cag tcc aaa gga   98
Val Leu Gly Leu Leu Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly
             15                  20                  25

gta gat cta ggc ttg tgt gat gaa acg agg ttc gag tgt aag tgt ggc   146
Val Asp Leu Gly Leu Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly
         30                  35                  40

gat cca ggc tat gtg ttc aac att cca gtg aaa caa tgt aca tac ttt   194
Asp Pro Gly Tyr Val Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe
     45                  50                  55

tat cga tgg agg ccg tat tgt aaa cca tgt gat gac ctg gag gct aag   242
Tyr Arg Trp Arg Pro Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys
 60                  65                  70                  75

gat att tgt cca aag tac aaa cga tgt caa gag tgt aag gct ggt ctt   290
Asp Ile Cys Pro Lys Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu
                 80                  85                  90
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gat agt tgt gtt act tgt cca cct aac aaa tat ggt act tgg tgt agc   338
Asp Ser Cys Val Thr Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser
             95                  100                 105

ggt gaa tgt cag tgt aag aat gga ggt atc tgt gac cag agg aca gga   386
Gly Glu Cys Gln Cys Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly
        110                 115                 120

gct tgt gca tgt cgt gac aga tat gaa ggg gtg cac tgt gaa att ctc   434
Ala Cys Ala Cys Arg Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu
    125                 130                 135

aaa ggt tgt cct ctt ctt cca tcg gat tct cag gtt cag gaa gtc aga   482
Lys Gly Cys Pro Leu Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg
140                 145                 150                 155

aat cca cca gat aat ccc caa act att gac tac agc tgt tca cca ggg   530
Asn Pro Pro Asp Asn Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly
                160                 165                 170

ttc aag ctt aag ggt atg gca cga att agc tgt ctc cca aat gga cag   578
Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln
            175                 180                 185

tgg agt aac ttt cca ccc aaa tgt att cga gaa tgt gcc atg gtt tca   626
Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser
        190                 195                 200

tct cca gaa cat ggg aaa gtg aat gct ctt agt ggt gat atg ata gaa   674
Ser Pro Glu His Gly Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu
    205                 210                 215

ggg gct act tta cgg ttc tca tgt gat agt ccc tac tac ttg att ggt   722
Gly Ala Thr Leu Arg Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly
220                 225                 230                 235

caa gaa aca tta acc tgt cag ggt aat ggt cag tgg aat gga cag ata   770
Gln Glu Thr Leu Thr Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile
                240                 245                 250

cca caa tgt aag aac ttg gtc ttc tgt cct gac ctg gat cct gta aac   818
Pro Gln Cys Lys Asn Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn
            255                 260                 265

cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat ggt cag   866
His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln
        270                 275                 280

ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac tac ttc   914
Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe
    285                 290                 295

ttg atg ggt ttt gac acc tta aaa tgt aac cct gat ggg tct tgg tca   962
Leu Met Gly Phe Asp Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser
300                 305                 310                 315

gga tca cag cca tcc tgt gtt aaa gtg gca gac aga gag gtc gac tgt  1010
Gly Ser Gln Pro Ser Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys
                320                 325                 330
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gac agt aaa gct gta gac ttc ttg gat gat gtt ggt gaa cct gtc agg   1058
Asp Ser Lys Ala Val Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg
            335                 340                 345

atc cac tgt cct gct ggc tgt tct ttg aca gct ggt act gtg tgg ggt   1106
Ile His Cys Pro Ala Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly
        350                 355                 360

aca gcc ata tac cat gaa ctt tcc tca gtg tgt cgt gca gcc atc cat   1154
Thr Ala Ile Tyr His Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His
    365                 370                 375

gct ggc aag ctt cca aac tct gga gga gcg gtg cat gtt gtg aac aat   1202
Ala Gly Lys Leu Pro Asn Ser Gly Gly Ala Val His Val Val Asn Asn
380                 385                 390                 395

ggc ccc tac tcg gac ttt ctg ggt agt gac ctg aat ggg ata aaa tcg   1250
Gly Pro Tyr Ser Asp Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser
                400                 405                 410

gaa gag ttg aag tct ctt gcc cgg agt ttc cga ttc gat tat gtc cgt   1298
Glu Glu Leu Lys Ser Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg
            415                 420                 425

tcc tcc aca gca ggt aaa tca gga tgt cct gat gga tgg ttt gag gta   1346
Ser Ser Thr Ala Gly Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val
        430                 435                 440

gac gag aac tgt gtg tac gtt aca tca aaa cag aga gcc tgg gaa aga   1394
Asp Glu Asn Cys Val Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg
    445                 450                 455

gct caa ggt gtg tgt acc aat atg gct gct cgt ctt gct gtg ctg gac   1442
Ala Gln Gly Val Cys Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp
460                 465                 470                 475

aaa gat gta att cca aat tcg ttg act gag act cta cga ggg aaa ggg   1490
Lys Asp Val Ile Pro Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly
                480                 485                 490

tta aca acc acg tgg ata gga ttg cac aga cta gat gct gag aag ccc   1538
Leu Thr Thr Thr Trp Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro
            495                 500                 505

ttt att tgg gag tta atg gat cgt agt aat gtg gtt ctg aat gat aac   1586
Phe Ile Trp Glu Leu Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn
        510                 515                 520
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cta aca ttc tgg gcc tct ggc gaa cct gga aat gaa act aac tgt gta   1634
Leu Thr Phe Trp Ala Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val
    525                 530                 535

tat atg gac atc caa gat cag ttg cag tct gtg tgg aaa acc aag tca   1682
Tyr Met Asp Ile Gln Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser
540                 545                 550                 555

tgt ttt cag ccc tca agt ttt gct tgc atg atg gat ctg tca gac aga   1730
Cys Phe Gln Pro Ser Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg
                560                 565                 570

aat aaa gcc aaa tgc gat gat cct gga tca ctg gaa aat gga cac gcc   1778
Asn Lys Ala Lys Cys Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala
            575                 580                 585

aca ctt cat gga caa agt att gat ggg ttc tat gct ggt tct tct ata   1826
Thr Leu His Gly Gln Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile
        590                 595                 600

agg tac agc tgt gag gtt ctc cac tac ctc agt gga act gaa acc gta   1874
Arg Tyr Ser Cys Glu Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val
    605                 610                 615

act tgt aca aca aat ggc aca tgg agt gct cct aaa cct cga tgt atc   1922
Thr Cys Thr Thr Asn Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile
620                 625                 630                 635

aaa gtc atc acc tgc caa aac ccc cct gta cca tca tat ggt tct gtg   1970
Lys Val Ile Thr Cys Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val
                640                 645                 650

gaa atc aaa ccc cca agt cgg aca aac tcg ata agt cgt gtt ggg tca   2018
Glu Ile Lys Pro Pro Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser
            655                 660                 665

cct ttc ttg agg ttg cca cgg tta ccc ctc cca tta gct aga gca gcc   2066
Pro Phe Leu Arg Leu Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala
        670                 675                 680

aaa cct cct cca aaa cct aga tcc tca caa ccc tct act gtg gac ttg   2114
Lys Pro Pro Pro Lys Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu
    685                 690                 695

gct tct aaa gtt aaa cta cct gaa ggt cat tac cgg gta ggg tct cga   2162
Ala Ser Lys Val Lys Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg
700                 705                 710                 715

gcc atc tac acg tgc gag tcg aga tac tac gaa cta ctt gga tct caa   2210
Ala Ile Tyr Thr Cys Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln
                720                 725                 730

ggc aga aga tgt gac tct aat gga aac tgg agt ggt cgg cca gcg agc   2258
Gly Arg Arg Cys Asp Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser
            735                 740                 745
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tgt att cca gtt tgt gga cgg tca gac tct cct cgt tct cct ttt atc   2306
Cys Ile Pro Val Cys Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile
        750                 755                 760

tgg aat ggg aat tct aca gaa ata ggt cag tgg ccg tgg cag gca gga   2354
Trp Asn Gly Asn Ser Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly
    765                 770                 775

atc tct aga tgg ctt gca gac cac aat atg tgg ttt ctc cag tgt gga   2402
Ile Ser Arg Trp Leu Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly
780                 785                 790                 795

gga tct cta ttg aat gag aaa tgg atc gtc act gct gcc cac tgt gtc   2450
Gly Ser Leu Leu Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val
                800                 805                 810

acc tac tct gct act gct gag att att gac ccc aat cag ttt aaa atg   2498
Thr Tyr Ser Ala Thr Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met
            815                 820                 825

tat ctg ggc aag tac tac cgt gat gac agt aga gac gat gac tat gta   2546
Tyr Leu Gly Lys Tyr Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val
        830                 835                 840

caa gta aga gag gct ctt gag atc cac gtg aat cct aac tac gac ccc   2594
Gln Val Arg Glu Ala Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro
    845                 850                 855

ggc aat ctc aac ttt gac ata gcc cta att caa ctg aaa act cct gtt   2642
Gly Asn Leu Asn Phe Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val
860                 865                 870                 875

act ttg aca aca cga gtc caa cca atc tgt ctg cct act gac atc aca   2690
Thr Leu Thr Thr Arg Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr
                880                 885                 890

aca aga gaa cac ttg aag gag gga aca tta gca gtg gtg aca ggt tgg   2738
Thr Arg Glu His Leu Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp
            895                 900                 905

ggt ttg aat gaa aac aac acc tat tca gag acg att caa caa gct gtg   2786
Gly Leu Asn Glu Asn Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val
        910                 915                 920

cta cct gtt gtt gca gcc agc acc tgt gaa gag ggg tac aag gaa gca   2834
Leu Pro Val Val Ala Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala
    925                 930                 935

gac tta cca ctg aca gta aca gag aac atg ttc tgt gca ggt tac aag   2882
Asp Leu Pro Leu Thr Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys
940                 945                 950                 955

aag gga cgt tat gat gcc tgc agt ggg gac agt gga gga cct tta gtg   2930
Lys Gly Arg Tyr Asp Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val
                960                 965                 970
```

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ttt gct gat gat tcc cgt acc gaa agg cgg tgg gtc ttg gaa ggg att   2978
Phe Ala Asp Asp Ser Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile
            975                 980                 985

gtc agc tgg ggc agt ccc agt gga tgt ggc aag gcg aac cag tac ggg   3026
Val Ser Trp Gly Ser Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly
        990                 995                1000

ggc ttc act aaa gtt aac gtt ttc ctg tca tgg att agg cag ttc att   3074
Gly Phe Thr Lys Val Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
   1005                1010                1015

tgaaactgat ctaaatattt taagcatggt tataaacgtc ttgtttccta ttattgcttt 3134

actagtttaa cccataagaa ggttaactgg gtaaggcaca aggatcattg tttctgtttg 3194

tttttacaaa tggttatttt agtcagtgaa tgagaatagt atccattgaa gactgttacc 3254

ttttattcta ccttttttata ttactatgta agtatttggg atatcttcta cacatgaaaa 3314

ttctgtcatt ttaccataaa tttggtttct ggtgtgtgct aagtccacca gtagagaacg 3374

atgtaatttt cactagcaca tgaaataaat atagaacaaa tctattataa actaccttaa 3434

aaaaaaaaaa aaaa                                                   3448
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<213> Carcinoscorpius rotundicauda

<400> 6

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Met Val Leu Ala Ser Phe Leu Val Ser Gly Leu Val Leu Gly Leu Leu
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Ala Gln Lys Met Arg Pro Val Gln Ser Lys Gly Val Asp Leu Gly Leu
            20                  25                  30

Cys Asp Glu Thr Arg Phe Glu Cys Lys Cys Gly Asp Pro Gly Tyr Val
        35                  40                  45

Phe Asn Ile Pro Val Lys Gln Cys Thr Tyr Phe Tyr Arg Trp Arg Pro
    50                  55                  60

Tyr Cys Lys Pro Cys Asp Asp Leu Glu Ala Lys Asp Ile Cys Pro Lys
65                  70                  75                  80

Tyr Lys Arg Cys Gln Glu Cys Lys Ala Gly Leu Asp Ser Cys Val Thr
                85                  90                  95

Cys Pro Pro Asn Lys Tyr Gly Thr Trp Cys Ser Gly Glu Cys Gln Cys
            100                 105                 110

Lys Asn Gly Gly Ile Cys Asp Gln Arg Thr Gly Ala Cys Ala Cys Arg
        115                 120                 125

Asp Arg Tyr Glu Gly Val His Cys Glu Ile Leu Lys Gly Cys Pro Leu
    130                 135                 140
```

```
Leu Pro Ser Asp Ser Gln Val Gln Glu Val Arg Asn Pro Pro Asp Asn
145                 150                 155                 160

Pro Gln Thr Ile Asp Tyr Ser Cys Ser Pro Gly Phe Lys Leu Lys Gly
                165                 170                 175

Met Ala Arg Ile Ser Cys Leu Pro Asn Gly Gln Trp Ser Asn Phe Pro
            180                 185                 190

Pro Lys Cys Ile Arg Glu Cys Ala Met Val Ser Ser Pro Glu His Gly
        195                 200                 205

Lys Val Asn Ala Leu Ser Gly Asp Met Ile Glu Gly Ala Thr Leu Arg
    210                 215                 220

Phe Ser Cys Asp Ser Pro Tyr Tyr Leu Ile Gly Gln Glu Thr Leu Thr
225                 230                 235                 240

Cys Gln Gly Asn Gly Gln Trp Asn Gly Gln Ile Pro Gln Cys Lys Asn
                245                 250                 255

Leu Val Phe Cys Pro Asp Leu Asp Pro Val Asn His Ala Glu His Lys
            260                 265                 270

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
        275                 280                 285

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Gly Phe Asp
    290                 295                 300

Thr Leu Lys Cys Asn Pro Asp Gly Ser Trp Ser Gly Ser Gln Pro Ser
305                 310                 315                 320

Cys Val Lys Val Ala Asp Arg Glu Val Asp Cys Asp Ser Lys Ala Val
                325                 330                 335

Asp Phe Leu Asp Asp Val Gly Glu Pro Val Arg Ile His Cys Pro Ala
            340                 345                 350

Gly Cys Ser Leu Thr Ala Gly Thr Val Trp Gly Thr Ala Ile Tyr His
        355                 360                 365

Glu Leu Ser Ser Val Cys Arg Ala Ala Ile His Ala Gly Lys Leu Pro
    370                 375                 380

Asn Ser Gly Gly Ala Val His Val Val Asn Asn Gly Pro Tyr Ser Asp
385                 390                 395                 400

Phe Leu Gly Ser Asp Leu Asn Gly Ile Lys Ser Glu Glu Leu Lys Ser
                405                 410                 415

Leu Ala Arg Ser Phe Arg Phe Asp Tyr Val Arg Ser Ser Thr Ala Gly
            420                 425                 430

Lys Ser Gly Cys Pro Asp Gly Trp Phe Glu Val Asp Glu Asn Cys Val
        435                 440                 445

Tyr Val Thr Ser Lys Gln Arg Ala Trp Glu Arg Ala Gln Gly Val Cys
    450                 455                 460
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```
Thr Asn Met Ala Ala Arg Leu Ala Val Leu Asp Lys Asp Val Ile Pro
465                 470                 475                 480

Asn Ser Leu Thr Glu Thr Leu Arg Gly Lys Gly Leu Thr Thr Thr Trp
                485                 490                 495

Ile Gly Leu His Arg Leu Asp Ala Glu Lys Pro Phe Ile Trp Glu Leu
            500                 505                 510

Met Asp Arg Ser Asn Val Val Leu Asn Asp Asn Leu Thr Phe Trp Ala
        515                 520                 525

Ser Gly Glu Pro Gly Asn Glu Thr Asn Cys Val Tyr Met Asp Ile Gln
    530                 535                 540

Asp Gln Leu Gln Ser Val Trp Lys Thr Lys Ser Cys Phe Gln Pro Ser
545                 550                 555                 560

Ser Phe Ala Cys Met Met Asp Leu Ser Asp Arg Asn Lys Ala Lys Cys
                565                 570                 575

Asp Asp Pro Gly Ser Leu Glu Asn Gly His Ala Thr Leu His Gly Gln
            580                 585                 590

Ser Ile Asp Gly Phe Tyr Ala Gly Ser Ser Ile Arg Tyr Ser Cys Glu
        595                 600                 605

Val Leu His Tyr Leu Ser Gly Thr Glu Thr Val Thr Cys Thr Thr Asn
    610                 615                 620

Gly Thr Trp Ser Ala Pro Lys Pro Arg Cys Ile Lys Val Ile Thr Cys
625                 630                 635                 640

Gln Asn Pro Pro Val Pro Ser Tyr Gly Ser Val Glu Ile Lys Pro Pro
                645                 650                 655

Ser Arg Thr Asn Ser Ile Ser Arg Val Gly Ser Pro Phe Leu Arg Leu
            660                 665                 670

Pro Arg Leu Pro Leu Pro Leu Ala Arg Ala Ala Lys Pro Pro Pro Lys
        675                 680                 685

Pro Arg Ser Ser Gln Pro Ser Thr Val Asp Leu Ala Ser Lys Val Lys
    690                 695                 700

Leu Pro Glu Gly His Tyr Arg Val Gly Ser Arg Ala Ile Tyr Thr Cys
705                 710                 715                 720

Glu Ser Arg Tyr Tyr Glu Leu Leu Gly Ser Gln Gly Arg Arg Cys Asp
                725                 730                 735

Ser Asn Gly Asn Trp Ser Gly Arg Pro Ala Ser Cys Ile Pro Val Cys
            740                 745                 750

Gly Arg Ser Asp Ser Pro Arg Ser Pro Phe Ile Trp Asn Gly Asn Ser
        755                 760                 765

Thr Glu Ile Gly Gln Trp Pro Trp Gln Ala Gly Ile Ser Arg Trp Leu
    770                 775                 780
```

```
Ala Asp His Asn Met Trp Phe Leu Gln Cys Gly Gly Ser Leu Leu Asn
785                 790                 795                 800

Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Thr Tyr Ser Ala Thr
                805                 810                 815

Ala Glu Ile Ile Asp Pro Asn Gln Phe Lys Met Tyr Leu Gly Lys Tyr
            820                 825                 830

Tyr Arg Asp Asp Ser Arg Asp Asp Asp Tyr Val Gln Val Arg Glu Ala
        835                 840                 845

Leu Glu Ile His Val Asn Pro Asn Tyr Asp Pro Gly Asn Leu Asn Phe
    850                 855                 860

Asp Ile Ala Leu Ile Gln Leu Lys Thr Pro Val Thr Leu Thr Thr Arg
865                 870                 875                 880

Val Gln Pro Ile Cys Leu Pro Thr Asp Ile Thr Thr Arg Glu His Leu
                885                 890                 895

Lys Glu Gly Thr Leu Ala Val Val Thr Gly Trp Gly Leu Asn Glu Asn
            900                 905                 910

Asn Thr Tyr Ser Glu Thr Ile Gln Gln Ala Val Leu Pro Val Val Ala
        915                 920                 925

Ala Ser Thr Cys Glu Glu Gly Tyr Lys Glu Ala Asp Leu Pro Leu Thr
    930                 935                 940

Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Lys Lys Gly Arg Tyr Asp
945                 950                 955                 960

Ala Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Phe Ala Asp Asp Ser
                965                 970                 975

Arg Thr Glu Arg Arg Trp Val Leu Glu Gly Ile Val Ser Trp Gly Ser
            980                 985                 990

Pro Ser Gly Cys Gly Lys Ala Asn Gln Tyr Gly Gly Phe Thr Lys Val
        995                1000                1005

Asn Val Phe Leu Ser Trp Ile Arg Gln Phe Ile
   1010                1015
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<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> rS3-1mer

<400> 7

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Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr Gly
  1               5                  10                  15
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Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr
            20                  25                  30

Phe Leu Met Asp
        35
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<210> 8
<211> 468
<212> DNA
<213> Artificial Sequence

<220>
<223> rS3-4mer

<400> 8

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ccc cag gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa      48
Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
1               5                   10                  15

aaa tat ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg      96
Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
            20                  25                  30

ggt aac tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag     144
Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
        35                  40                  45

gtt aaa att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act     192
Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
    50                  55                  60

gaa gtg acc tat acg tgt tcg ggt aac tac ttc ttg atg gac ccc cag     240
Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65                  70                  75                  80

gat ccc cat gct gaa cac aag gtt aaa att ggt gtg gaa caa aaa tat     288
Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
                85                  90                  95

ggt cag ttt cct caa ggc act gaa gtg acc tat acg tgt tcg ggt aac     336
Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
            100                 105                 110

tac ttc ttg atg gac ccc cag gat ccc cat gct gaa cac aag gtt aaa     384
Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
        115                 120                 125

att ggt gtg gaa caa aaa tat ggt cag ttt cct caa ggc act gaa gtg     432
Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
    130                 135                 140

acc tat acg tgt tcg ggt aac tac ttc ttg atg gac                     468
Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145                 150                 155
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<210> 9
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> rS3-4mer

<400> 9

Pro Gln Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln
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Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser
20 25 30

Gly Asn Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys
35 40 45

Val Lys Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr
50 55 60

Glu Val Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp Pro Gln
65 70 75 80

Asp Pro His Ala Glu His Lys Val Lys Ile Gly Val Glu Gln Lys Tyr
85 90 95

Gly Gln Phe Pro Gln Gly Thr Glu Val Thr Tyr Thr Cys Ser Gly Asn
100 105 110

Tyr Phe Leu Met Asp Pro Gln Asp Pro His Ala Glu His Lys Val Lys
115 120 125

Ile Gly Val Glu Gln Lys Tyr Gly Gln Phe Pro Gln Gly Thr Glu Val
130 135 140

Thr Tyr Thr Cys Ser Gly Asn Tyr Phe Leu Met Asp
145 150 155